



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 130569

TO: Ilia Ouspenski
Location: 3d74 / 3c70
Tuesday, August 24, 2004
Art Unit: 1644
Phone: 272-2920
Serial Number: 09 / 888324

From: Jan Delaval
Location: Biotech-Chem Library
Rem 1A51
Phone: 272-2504

jan.delaval@uspto.gov

Search Notes

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
Art Unit: _____ Phone Number 30 _____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u>an</u>	NA Sequence (#) _____	STN _____
Searcher Phone #: <u>22504</u>	AA Sequence (#) <input checked="" type="checkbox"/>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>8/24</u>	Bibliographic _____	Dr. Link _____
Date Completed: <u>8/24</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/>
Clerical Prep Time: <u>60</u>	Patent Family _____	WWW/Internet _____
Online Time: <u>10</u>	Other _____	Other (specify) _____

130569

Delaval, Jan

From: Ouspenski, Ilia
Sent: Tuesday, August 24, 2004 10:00 AM
To: Delaval, Jan
Subject: sequence search for 09/888,324

Dear Jan,

Please provide polypeptide search for SEQ ID NO:66 for 09888324.

Thanks,

Ilia

ILIA OUSPENSKI, Ph.D.
Examiner
Art Unit 1644
Phone: 571-272-2920
REM 3D74
Mailstop 3c70

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OM protein - protein search, using sw model

Run on: August 24, 2004, 10:18:46 / Search time 116 Seconds

(without alignments)
824.155 Million cell updates/sec

Title: US-09-888-324-66

Perfect score: 1613
Sequence: 1 MGHMKWGLPPKRCPLWLS.....FTVGTERTLSPYLGASQSSG 303

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SPTREMBL 25:*

- 1: sp.archaea:*
- 2: sp.bacteria:*
- 3: sp.fungi:*
- 4: sp.human:*
- 5: sp.invertebrate:*
- 6: sp.mammal:*
- 7: sp.mhc:*
- 8: sp.organelle:*
- 9: sp.phage:*
- 10: sp.plant:*
- 11: sp.podent:*
- 12: sp.virus:*
- 13: sp.vertebrate:*
- 14: sp.unclassified:*
- 15: sp.virus:*
- 16: sp.bacterioph:*
- 17: sp.archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1262.5	78.3	296	6	Q6405
2	962	59.6	296	6	Q6M22
3	944.5	58.6	297	6	Q8B39
4	930.5	57.0	304	6	Q8TQX1
5	919	57.0	292	6	Q02758
6	912	56.5	292	6	Q9GMZ8
7	902.5	56.0	288	6	Q9TT70
8	864	53.6	230	6	Q9N213
9	862	53.4	229	6	Q9TT71
10	830	51.5	288	6	Q77684
11	811	50.3	288	6	Q28499
12	802.5	49.8	235	6	Q9TQ68
13	800	49.6	288	6	Q9BDN6
14	800	49.6	289	6	Q28347
15	792.5	49.1	235	6	Q9N070
16	691.5	42.9	294	11	Q8B36

17	665	41.2	321	11	Q35187	Q35187 rattus norv
18	665	41.2	321	11	Q55202	Q55202 rattus norv
19	661	41.0	321	11	Q62624	Q62624 rattus norv
20	657	40.7	290	11	Q62680	Q62680 rattus norv
21	641	39.7	292	11	Q80W97	Q80W97 meriones un
22	639	39.6	306	11	Q9R129	Q9R129 mus musculu
23	442	27.4	173	6	Q95L17	Q95L17 fells silve
24	434.5	26.9	174	6	Q9GMZ9	Q9GMZ9 fells silve
25	278	17.2	212	11	Q61332	Q61332 mus musculu
26	230	14.4	323	6	Q9BDN9	Q9BDN9 macaca neme
27	230	14.3	323	6	Q9BDN8	Q9BDN8 cercocobus
28	230	14.3	323	6	Q9BDN4	Q9BDN4 macaca mula
29	230	14.3	329	6	Q9XG36	Q9XG36 fells silve
30	230	14.3	332	6	Q9GMZ7	Q9GMZ7 fells silve
31	230	14.3	332	6	Q95L16	Q95L16 fells silve
32	217	13.5	323	6	Q9BDN2	Q9BDN2 cercocobus
33	203	12.6	329	6	Q9TIF2	Q9TIF2 canis fami
34	201	12.5	284	6	Q9GL33	Q9GL33 bos taurus
35	199.5	12.4	325	6	Q02838	Q02838 sus scrofa
36	193	12.0	314	11	Q61238	Q61238 mus musculu
37	193	12.0	326	11	Q64381	Q64381 mus musculu
38	192	11.9	281	11	Q6CT88	Q6CT88 mesocricetu
39	191	11.8	289	11	Q8KJ33	Q8KJ33 meriones un
40	190	11.8	289	6	Q9TIF1	Q9TIF1 canis fami
41	190	11.8	309	11	Q91YV7	Q91YV7 mus musculu
42	189	11.7	313	11	Q35531	Q35531 rattus norv
43	180.5	11.2	275	6	Q9BDN9	Q9BDN9 papio anubi
44	179.5	11.1	296	13	Q42404	Q42404 gallus gall
45	153.5	9.5	316	11	Q7PBP4	Q7PBP4 rattus norv

ALIGNMENTS

RESULT 1

ID	Q6405	PRELIMINARY;	PRT;	296 AA.
AC	Q6405			
DT	01-JUN-1998 (TREMBLrel. 06, Created)			
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	CD80 anitgen precursor (Fragment).			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99115507; PubMed=9914337;			
RA	Parsons K.R., Howard C.;			
RT	"Cloning of cattle CD80."			
RL	Immunogenetics 49:231-234 (1999).			
DR	EMBL; Y09950; CAA71081.1; -			
DR	HSSP; P33681; ID89.			
DR	InterPro; IPR003589; IG.			
DR	InterPro; IPR007110; IG-like.			
DR	Fram; PFO0047; IG; 2.			
DR	SMART; SM00409; IG; 1.			
DR	PROSITE; PS50835; IG_LIKE; 2.			
KW	signal.			
FT	SIGNAL.			
FT	NON TER			
FT	SEQUENCE			

Query Match 78.3%; Score 1262.5; DB 6; Length 296;
Best Local Similarity 81.8%; Pred. No. 1.9e-112;
Matches 242; Conservative 19; Mismatches 32; Indels 3; Gaps 2;

QY 1 MGHMKWGLPPKRCPLWLSQILVLTGLFPGSGITPKSVTKRVKVTMLSCDINTSTEE 60
DB 1 MGHMKWGLPPKRCPLWLSQILVLTGLFPGSGITPKSVTKRVKVTMLSCDINTSTEE 60

March 1999

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QY 61 LTRIRIYOKDSKXVIALIPGKVQWPEYKRNRTITMDNPRIVIALRPSDGTTCVI 120
DB 61 LTRIRIYOKDSKXVIALIPGKVQWPEYKRNRTITMDNPRIVIALRPSDGTTCVI 120
QY 121 QKPLKGAAYLEHLASVRLMIRADFPVPTINDIGNPSPNIRLICSTSGGFPRLHYME 180
DB 121 QKPLKGAAYLEHLASVRLMIRADFPVPTINDIGNPSPNIRLICSTSGGFPRLHYME 180
QY 181 NGEELNATNTTTSQDPETELYMISSELDENVNTHNSIVCLIKYGEISVSQIFPWSKPKQE 240
DB 181 NGEELNATNTTTSQDPETELYMISSELDENVNTHNSIVCLIKYGEISVSQIFPWSKPKQE 240
QY 241 PFIDOLPEFW-VIFPVS--GALVLTAVLYCLACRHVARMKRTTRNEETVTEELSP 293
DB 241 PFIDOLPEFW-VIFPVS--GALVLTAVLYCLACRHVARMKRTTRNEETVTEELSP 293

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21/208=

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RESULT 2
Q8MWZ2 PRELIMINARY; PRT; 296 AA.
ID Q8MWZ2;
AC Q8MWZ2;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DN CD80.
GN CD80.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Tadaki D.K., Williams A., Lee K.P., Kirk A.D., Harlan D.M.;
RT "Porcine CD80: Cloning, characterization and evidence for its role in
RT direct human T-cell activation";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF45811; AAL58443.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PSS0835; IG-like; 2.
SQ SEQUENCE 296 AA; 33275 MW; 69E494237E79C98 CRC64;

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Query Match 59.6%; Score 962; DB 6; Length 296;
Best Local Similarity 63.6%; Pred. No. 1,le-83;
Matches 194; Conservative 36; Mismatches 63; Indels 12; Gaps 5;

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QY 1 MGHTRKMGSLPPKRPCLMLTGLVGLFGSGITPKSVTKRYKRTWMLSCDYNSTEE 60
DB 1 MGHTRKMGSLPPKRPCLMLTGLVGLFGSGITPKSVTKRYKRTWMLSCDYNSTEE 60
QY 61 LTRIRIYOKDSKXVIALIPGKVQWPEYKRNRTITMDNPRIVIALRPSDGTTCVI 120
DB 61 LTRIRIYOKDSKXVIALIPGKVQWPEYKRNRTITMDNPRIVIALRPSDGTTCVI 120
QY 121 QKPLKGAAYLEHLASVRLMIRADFPVPTINDIGNPSPNIRLICSTSGGFPRLHYME 180
DB 121 QKPLKGAAYLEHLASVRLMIRADFPVPTINDIGNPSPNIRLICSTSGGFPRLHYME 180
QY 181 NGEELNATNTTTSQDPETELYMISSELDENVNTHNSIVCLIKYGEISVSQIFPWSKPKQE 240
DB 181 NGEELNATNTTTSQDPETELYMISSELDENVNTHNSIVCLIKYGEISVSQIFPWSKPKQE 240
QY 241 PFIDOLPEFW-VIFPVS--GALVLTAVLYCLACRHVARMKRTTRNEETVTEELSP 293
DB 241 PFIDOLPEFW-VIFPVS--GALVLTAVLYCLACRHVARMKRTTRNEETVTEELSP 293
QY 299 AQSOG 303
DB 299 AQSOG 303
QY 291 VEGPG 295
DB 291 VEGPG 295

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RESULT 3
Q9BE99 PRELIMINARY; PRT; 297 AA.
ID Q9BE99;
AC Q9BE99;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DN CD80 protein precursor.
GN CD80/B7-1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Wade M., Amas S., Sano N., Ishii T., Hoshi M., Sasaki H., Nio M.,
RA Hayashi Y., Shi R.;
RT "Cloning and sequencing of cDNAs for porcine B7-1 (CD80) and soluble
RT isoforms";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049760; BAB40952.1; -
DR HSP; P33681; ID99.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PSS0835; IG-like; 2.
FT CHAIN 1 POTENTIAL.
FT SIGNAL 29 CD80 PROTEIN.
SQ SEQUENCE 297 AA; 33438 MW; 23109711EA63EF23 CRC64;

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Query Match 58.6%; Score 944.5; DB 6; Length 297;
Best Local Similarity 62.7%; Pred. No. 5,4e-82;
Matches 192; Conservative 38; Mismatches 63; Indels 13; Gaps 6;

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QY 1 MGHTRKMGSLPPKRPCLMLTGLVGLFGSGITPKSVTKRYKRTWMLSCDYNSTEE 60
DB 1 MGHTRKMGSLPPKRPCLMLTGLVGLFGSGITPKSVTKRYKRTWMLSCDYNSTEE 60
QY 61 LTRIRIYOKDSKXVIALIPGKVQWPEYKRNRTITMDNPRIVIALRPSDGTTCVI 120
DB 61 LTRIRIYOKDSKXVIALIPGKVQWPEYKRNRTITMDNPRIVIALRPSDGTTCVI 120
QY 121 QKPLKGAAYLEHLASVRLMIRADFPVPTINDIGNPSPNIRLICSTSGGFPRLHYME 180
DB 121 QKPLKGAAYLEHLASVRLMIRADFPVPTINDIGNPSPNIRLICSTSGGFPRLHYME 180
QY 181 NGEELNATNTTTSQDPETELYMISSELDENVNTHNSIVCLIKYGEISVSQIFPWSKPKQE 240
DB 181 NGEELNATNTTTSQDPETELYMISSELDENVNTHNSIVCLIKYGEISVSQIFPWSKPKQE 240
QY 241 PFIDOLPEFW-VIFPVS--GALVLTAVLYCLACRHVARMKRTTRNEETVTEELSP 293
DB 241 PFIDOLPEFW-VIFPVS--GALVLTAVLYCLACRHVARMKRTTRNEETVTEELSP 293
QY 299 AQSOG 303
DB 299 AQSOG 303
QY 291 VEGPG 296
DB 291 VEGPG 296

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